

STIC-Biot ch/ChemLib

From: Chernyshev, Olga
Sent: Wednesday, August 21, 2002 11:01 AM
To: STIC-Biotech/ChemLib
Subject: sequence search request

**Please search US case 09/462,909 SEQ ID NO: 7.
Thank you very much!**

*Olga N. Chernyshev
AU1646
CM1 10E18
305-1003
mail box 10C01*

D19

Point of Contact:
Alexandra Wacławiw
Technical Info. Specialist
CM1 6A02 Tel: 305-441

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 8122
Date Completed: 8122
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: 1 _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): campus

us-09-462-909d-7.rsp

```

Query Match      91.9% Score 57; DB 1; Length 1077;
Best Local Similarity 66.7%; Pred. No. 0.079;
Matches      8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY      1 WSWSKSCXXCG 12
        ||| ||| |||
DB       847 WWSWKSCTATCG 858

RESULT      2
SSPO_BOVIN
ID          SSPO_BOVIN      STANDARD; PRT; 867 AA.
AC          P99167;
DT          01-OCT-1996 (Rel. 34, Created)
DT          01-OCT-1996 (Rel. 34, Last sequence update)
DT          16-OCT-2001 (Rel. 40, Last annotation update)
DS          SCQ-spodlin, Fragment).
OS          Bos taurus (Bovine).
OC          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC          Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC          Bovidae; Bovinae; Bos.
OX          NCBI_TaxID=9913;
RN          [1]
RS          SEQUENCE FROM N.A.
RC          TISSUE-Dependymocyte;
RX          MEDLINE=96338614; PubMed=8743952;
RA          Gobron S., Monnerie H., Meinzel R., Creveaux I., Lehmann W.,
RA          Lalleau D., Pastugue B., Meintzel A.;
RT          "SCQ-spodlin: a new member of the thropospondin family secreted by
RT          the subcommissural organ is a candidate in the modulation of neuronal
RT          aggregation."
RL          J. Cell Sci. 109:1053-1061(1996).
CC          -1- FUNCTION: INVOLVED IN THE MODULATION OF NEURONAL AGGREGATION.
CC          -1- SUBCELLULAR LOCATION: Extracellular.
CC          -1- TISSUE SPECIFICITY: SUBCOMMISSURAL ORGAN.
CC          -1- DEVELOPMENTAL STAGE: EMBRYO.
CC          -1- SIMILARITY: BELONGS TO THE THROMOSPONDIN FAMILY.
CC          -1- SIMILARITY: CONTAINS AT LEAST 2 ESP-LIKE DOMAINS.
CC          -1- SIMILARITY: CONTAINS AT LEAST 3 LDL-RECEPTOR CLASS A DOMAINS.
CC          -1- SIMILARITY: CONTAINS AT LEAST 3 LDL-RECEPTOR CLASS A DOMAINS.
CC          This SWISS-PROT entry is copyright. It is produced through a collaboration
CC          between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC          the European Bioinformatics Institute. There are no restrictions on its
CC          use by non-profit institutions as long as its content is in no way
CC          modified and this statement is not removed. Usage by and for commercial
CC          entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC          or send an email to license@sib-sib.ch).
DR          EMBL; X93922; CAA63815.1; -.
DR          HSSP; P01130; IAUJ.
DR          InterPro: IPRO000421; FA58.C.
DR          InterPro: IPRO02172; LDL_recept_A.
DR          InterPro: IPRO02919; TIL.
DR          InterPro: IPRO00884; TSF1.
DR          InterPro: IPRO01007; WMPC.
DR          Pfam: PF000754; F5_F8_type_C; 1.
DR          Pfam: PF00057; ldl_recept_c; 3.
DR          Pfam: PF01826; TIL; 1.
DR          Pfam: PF00090; tsp_1; 4.
DR          Pfam: PF00093; vwc; 1.
DR          SMART; SM00231; FA58C; 1.
DR          SMART; SM00192; LDIA; 3.
DR          SMART; SM00209; TSP1; 4.
DR          SMART; SM00214; VWC; 1.
DR          PROSITE; PS01285; FA58C_1; 1.
DR          PROSITE; PS01286; FA58C_2; 1.

```

DR PROSITE: PS01209; LIDRA_1; 3.
 DR PROSITE: PS50068; LIDRA_2; 3.
 DR PROSITE: PS50092; TSP1; 4.
 KM Glycoprotein; Cell adhesion; Calcium-binding; Repeat; EGF-like domain.
 FT NON_TER 1 1
 FT DOMAIN 26 141 TSP TYPE-1.1.
 FT DOMAIN 103 142 EGF-LIKE 1.
 FT DOMAIN 143 180 EGF-LIKE 2.
 FT DOMAIN 183 243 TSP TYPE-1.2.
 FT DOMAIN 344 502 TSP TYPE-1.3.
 FT DOMAIN 506 544 LDL-RECEPTOR CLASS A.1.
 FT DOMAIN 663 701 LDL-RECEPTOR CLASS A.2.
 FT DOMAIN 723 761 LDL-RECEPTOR CLASS A.3.
 FT DOMAIN 762 813 TSP TYPE-1.3.
 FT DOMAIN 814 867 TSP TYPE-1.4.
 FT DISULFID 107 122 BY SIMILARITY.
 FT DISULFID 116 127 BY SIMILARITY.
 FT DISULFID 129 141 BY SIMILARITY.
 FT DISULFID 147 166 BY SIMILARITY.
 FT DISULFID 149 169 BY SIMILARITY.
 FT DISULFID 171 179 BY SIMILARITY.
 FT DISULFID 344 502 BY SIMILARITY.
 FT DISULFID 508 520 BY SIMILARITY.
 FT DISULFID 515 533 BY SIMILARITY.
 FT DISULFID 527 532 BY SIMILARITY.
 FT DISULFID 627 677 BY SIMILARITY.
 FT DISULFID 672 690 BY SIMILARITY.
 FT DISULFID 684 699 BY SIMILARITY.
 FT DISULFID 725 737 BY SIMILARITY.
 FT DISULFID 732 750 BY SIMILARITY.
 FT DISULFID 744 759 BY SIMILARITY.
 FT CARBOHYD 88 88 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CARBOHYD 309 309 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CARBOHYD 409 409 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT NON_TER 867 867
 SQ SEQUENCE 867 AA; 91817 MW; 9538F2108E787B49 CRC64;
 Query Match 90.3%; Score 56; DB 1; Length 867;
 Best Local Similarity 66.7%; Pred. No. 0.094;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 WSXWSXCSXXCG 12
 Db 767 WSGNSGSRSG 778
 SUIT 3
 AT57_HUMAN STANDARD; PRT; 997 AA.
 ID AT57_HUMAN
 AC Q9UKP4;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE ADAMTS-7 Precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 7) (ADAM-TS 7) (ADAM-TS7).
 GN ADAMTS7.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9395124; PubMed=10464288;
 RA Hurskainen T.L., Hirohata S., Seldin M.F., Apte S.S.;
 FT "ADAM-TS5, ADAM-TS6, and ADAM-TS7, Novel Members of a New Family of
 FT Zinc Metalloproteinases";
 RL J. Biol. Chem. 274:25555-25563(1999).
 CC -1- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: SECRETED. ASSOCIATED WITH THE EXTRACELLULAR
 CC MATRIX (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, PLACENTA, LUNG,
 CC LIVER, SKELETAL MUSCLE, KIDNEY, PANCREAS.

CC -1- DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT
 CC FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.
 CC -1- PTM: THE PRECURSOR IS CLEAVED BY A FORIN ENDOPEPTIDASE (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
 CC -1- SIMILARITY: CONTRAINS 1 DISINTEGRIN-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTRAINS 2 TSP TYPE-1 DOMAINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC at the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: AF140675; MAD56358.1; -
 DR HSSP: P15167; IATL.
 DR MIM: 605009; -
 DR InterPro: IPR001762; Disintegrin.
 DR InterPro: IPR002870; Pep_M12B_propep.
 DR InterPro: IPR001590; Reptolysin.
 DR InterPro: IPR000884; TSP1.
 DR InterPro: IPR000130; zn_M12Bpeptidase.
 DR Pfam: PF01562; Pep_M12B_propep; 1.
 DR Pfam: PF01421; Reptolysin; 1.
 DR Pfam: PF00090; TSP1; 1.
 DR SMART: SM00209; TSP1; 2.
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 DR PROSITE: PS50215; ADAM_MEPRO; 1.
 DR PROSITE: PS50092; TSP1; 1.
 DR PROSITE: PS00427; DISINTEGRIN_1; FALSE NEG.
 KM Hydrolyase; Metalloproteinase; Zinc; Signal; Glycoprotein; Zymogen;
 KM Repeat; Extracellular matrix.
 FT SIGNAL 1 27
 FT PROPEP 28 232
 FT CHAIN 233 997
 FT SITE 204 204
 FT METAL 388 388
 FT ACT_SITE 389 389
 FT METAL 392 392
 FT METAL 398 398
 FT METAL 462 537
 FT DOMAIN 538 594
 FT DOMAIN 595 697
 FT DOMAIN 698 914
 FT DOMAIN 915 990
 FT CARBOHYD 94 94
 FT CARBOHYD 693 693
 FT CARBOHYD 778 778
 SQ SEQUENCE 997 AA; 109694 MW; 6587044ED02FC104 CRC64;
 Query Match 90.3%; Score 56; DB 1; Length 997;
 Best Local Similarity 66.7%; Pred. No. 0.11;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 WSXWSXCSXXCG 12
 Db 544 WSANSICSRSG 555
 RESULT 4
 BA13_HUMAN STANDARD; PRT; 1522 AA.
 ID BA13_HUMAN
 AC Q60242; Q60297;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Brain-specific angiogenesis inhibitor 3 precursor.
 GN BA13 OR KIA0550.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;